

TCGACCCACGCGTCCGGGAGGATCGGGAGTCCGGGAGGATGGGCCGCCGCTAGGCTCGCACTCCGGA
 CGCGCCTCGC
 AGTGCGCAGGGTGGGTGCCCCGCGCCTGCAGCGTCCGCCGGGGCGGCGCGGGAGGTGGCCGACAG
 GCTCCGGGCC
 TCGCAGCCTCAGCCCCCGGCCAGCGCGCTTTCCGACGGCGGGCGCGCCGAGCCACCCGCC
 CGCCCAAGGTCTCTCGCGGGCGGGAGAACCGGAAACTCCCAACTTCCTGAGTTCTAAAGTTCCTGTTG
 CTTTCAGACAA
 TGGATGAGCAATCACAAGGAATGCAAGGGCCACCTGTTCTCAGTTCCAACCACAGAAGGCCTTACGA
 CCGGATATGG
 GCTATAATACATTAGCCAACTTTTGAATAGAAAAGAAAATTGGTTCGCGGACAATTTAGTGAAG
 TTTATAGAGCAGCCTGTCTCTTGGATGGAGTACCAGTAGCTTTAAAAAAGTGCAGATATTTGATTTA
 ATGGATGCCA
 AAGCAGTGTCTGATTGCATCAAAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAA
 TATTATGCAT
 CATTCAATTGAAGATAATGAACTAAACATAGTTTTTGGAACTAGCAGATGCTGGCGACCTATCCA
 GAATGATCAAGCATTTTAAGAAGCAAAGAGGCTAATTCTGAAAGAACTGTTTGGAGTATTTTGT
 CAGCTTTGCA
 GTGCATTGGAACACATGCATTCTCGAAGAGTCATGCATAGAGATATAAAACCAGCTAATGTGTTTATT
 ACAGCCACTG
 GGGTGGTAAAACTTGGAGATCTTGGGCTTGGCCGGTTTTTCAGCTCAAAAACCACAGCTGCAC
 ATTCTTTAGTTGGTACGCCTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACCTCAA
 TCTGACATCT
 GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACAAAATGAAT
 TTATACTCAC
 TGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCTTCAGATCACTATTCAGAAGAAC
 TCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAGAGAAGCGACCAGACGTCACCTATGTTTAT
 GACGTAGCAA
 AGAGGATGCATGCATGCACTGCAAGCAGCTAAACATGCAAGATCATGAAGAGTGTAACCAAAGTAATT
 GAAAGTATTT
 TGTGCAAAGTCGTACCTSCCATTATGTCTGGGTGTTAAGATTAATATTTTTCAGAGCTAGTGT
 GCTCTGAATCCTTAACCAGTTTTTCATATAAGCTTCATTTTGTACCAGTCACCTAAATCACCTCCTTGC
 AACCCCCAA
 TGACTTTGGAATAACTGAATTGCATGTTAGGAGAGAAAATGAAACATGATGGTTTTGAATGGCTAAAG
 GTTTATAGAA
 TTTCTTACAGTTTTCTGCTGATAAATTGTGTTTAGATAGACTGTCAGTGCCAAATATTGAAGG
 TGCAGCTTGGCAGACATCAGAATAGACTCATACCTGAGAAAAGTATCTGAACATGTGACTTGTCTTCT
 TTTTATAGTAA
 TTTATGGACATTGAGATGAACACAATTGTGAACTTTTGTGAAGATTTTATTTTTTAAACGTTTGAAGTA
 CTAGTTTTAG
 TTCTTAGCAGAGTAGTTTTCAAATATGATTCTTATGATAAATGTAGACACAACTATTTGAGA
 AACATTTAGAACTCTTAGCTTATACATTCAAATGTAACCTATTAAATGTGAAGATTTGGGGACAAAT
 GTGAGTCAGA
 CACTGAAGAGTTTTTTGTTTTGTTTTAAATATTTTTTGATATTCTCTTGCATTGAAATGGTATAAATGA
 ATCCATTTAA
 AAAGTGGTTAAGGATTTGTTTATGCTGGTGTGATAATAATTTTTTAAAGTTGCACATTGCCCAAG
 GCTTTTTTTGTGTGTTTTATTGTTGTTTGTACATTTGAAAAATATTCTTTGAATAACCTTGCAGTAC
 TATATTTCAA

FIGURE 1

TTTCTTTATAAATTTAAGTGCATTTTAACTCATAATTGTACACTATAATATAAGCCTAAGTTTTTATT
 CATAAGTTTT
 ATTGAAGTTCTGATCGGTCCCCTTCAGAAATTTTTTTATATTATTCTTCAAGTTACTTTCTTA
 TTTATATTGTATGTGCATTTTATCCATTAATGTTTCATACTTTCTGAGAGTATAATACCCTTTTAAAA
 GATATTTGGT
 ATACCAATACTTTTCTGGATTGAAAACTTTTTTTAAACTTTTTTAAAATTTGGGCCACTCTGTATGCA
 TATGTTTGGT
 CTTGTTAAAGAGGAAGAAAGGATGTGTGTTATACTGTACCTGTGAATGTTGATACAGTTACAA
 TTTATTTGACAAGGTGTGAATCTAGAATATGCTTAATAAAATGAAAACCTGGCCATGACTACAGCCAG
 AACTGTTATG
 AGATTAACATTTCTATTGAGAAGCTTTTGAGTAAAGTACTGTATTTGTTTCATGAAGATGACTGAGATG
 GTAACACTTC
 GTGTAGCTTAAGGAAATGGGCAGAAATTCGTAAATGCTGTTGTGCAGATGTGTTTTCCCTGAA
 TGCTTTCGTATTAGTGGCGACCAGTTTCTCACAGAAATGTGAAGCCTGAAGGCCAAGAGGAAGTCACT
 GTTAAAGGAC
 TCTGTGCCATCTTACAACCTTGGATGAATTATCCTGCCAACGTGAAAACCTCATGTTCAAAGAACACT
 TCCCTTTAGC
 CGATGTAACCTGCTGGTTTTGTTTTTCATATGTGTTTTTCTTACACTCATTTGAATGCTTTCAA
 GCATTTGTAACTTAAAAAAANWAWAAAGGGCAAAAAGTCTGAACCCTTGTTTTCTGAAATCTAATC
 AGTTATGTAT
 GGTTTTCTGAAGGGTAATTTTATTTTGAATAGGTAAAGCGAAACCTGTTTTGTCWTGTTTTCTGAG
 GGCTAGATGC
 ATTTTTTTTCTCACACTCTTAATGACTTTTAAACATTTATACTGAGCATCCATAGATATATTC
 TAGAAGTATGAGAAGAATTATTCTTATTGACCATTAATGTGATGTTTCATTTTAATGTAATATAATTGA
 GATGAAATGT
 TCTCTGGTTGGAACAGATACTCTCTTTTTTTTTCTTGCAATCTTTAAGAATACATAGATCTAAAATTC
 ATTAGCTTGA
 CCCCTCAAAGTAACTTTTAAGTAAAGATTAAAGCTTTTCTTCTCAGTGAATATATCTGCTAGA
 AGGAAATAGCTGGGAAGAATTTAATGATCAGGGAAATTCATTATTTCTATATGTGGAACTTTTTGCT
 TCGAATATTG
 TATCTTTTTAAATCTAAATGTTTCATATTTTTCTGAAGAAACCACTGTGTAAAAATCAAATTTAATT
 TTGAATGGAA
 TAATTTCAAAGAACTATGAAGATGATTTGAAGCTCTAATTTATATAGTCACCTATAAAATGTT
 CTTTATATGTGTTTCATAAGTAAATTTTATATTGATTAAGTTAACTTTTGAATTGATTTGAGGAGCAG
 TAAAATGAAA
 GCTATATCTATTNCTAAACCYTATTTAGACATTGGKACCAGTTACCCAGGTGAAAATAKGGAGTAACT
 TTGTTTTGTA
 TGGTAAGGTTTAGGAATGGNGGATGAAGGGTATCTCTATATAAATAAAGTGCTCAACAATGTG
 CAATGATTGTAAATTTAGTAAGATATTACAGCCATTTTCATGAATGCTTTACCATTCAACATAGTATCT
 ATTACAAAAC
 ACCTTTCTTGATCCATATACTTCAGGTGTTGCTGTTAACATTTACTATGATATTTATTTTAACCAA
 ATGTTACTCA
 CATTAATGTTTATTCTTTTAAATGAATGTATTATGTTTTTAACCCACAAATGCATACTTACC
 CTGTGCCTCATATTTCAATAGTACTGTAATATGGACATCTTTGTGAAATACTTTTATTTTGTATGC
 TTTAAATATA
 CATACAAAAGATTTCTGTTATTAGCTTTGAAAATTGTATAATATCCTAATATAAACAAAAATATAAA
 AATAAAAATG
 AATACAGTAAAAAAAAAAAAAAAAAAAAAAAAAAGG

FIGURE 1 (cont'd)

MDEQSQGMQGPPVPQFQPKALRPDMGYNTLANFRIEKKIGRGQFSEVYRAACLLDGVPVALKKVQIF
DLMDAKARAD
CIKEIDLLKQLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYFVQLC
SALEHMHSSR
VMHRDIKPANVFITATGVVVLGDLGLGRFFSSKTTAAHSLVGTPYYMSPERIHENGYNFKSDI
WSLGCLLYEMAALQSPFYGDKMNLVSLCKKIEQCDYPPLPSDHYSEELRQLVNMCIINPDPEKRPDVTY
VYDVAKRMHA
CTASS

FIGURE 1 (cont'd)

3TCGACCCACGCGTCCGGTGAAGTATAATACTTTGTCAATTATGAGATGTCGTCTCTCGG
 TGCCTCCTTTGTGCAAATTAATTTGATGACTTGACAGTTTTTTGAAAACCTGCGGTGGAGG
 AAGTTTTGGGAGTGTATTATCGAGCCAAATGGATATCACAGGACAAGGAGGTGGCTGTAAA
 GAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTCAGTCACAGAAACAT
 CATCCAGTTTTATGGAGTAATTTCTTGAACCTCCCAACTATGGCATTGTACAGAATATGC
 TTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAGGAGATGGATATGGA
 TCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTATTTACATATGGAGGC
 TCCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGG
 AGTACTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAA TCATACAACACACATGTC
 CTTGGTTGGAACTTCCCATGGATGGCTCCAGAAGTTATCCAGAGTCTCCCTGTGTCAGA
 AACTTGTGACACATATTCTATGGTGTGGTTCTCTGGGAGATGCTAACAAGGGAGGTCCC
 CTTTAAAGGTTTGAAGGATTACAAGTAGCTTGGCTTGTAGTGGAAAAAACGAGAGATT
 AACCATTCCAAGCAGTTGCCCCAGAAGTTTTGCTGAACTGTTACATCAGTGTGGGAAGC
 TGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTTCAATCCTGGAGTCCATGTCAAA
 TGACACGAGCCTTCCTGACAAGTGTAACCTATTCCCTACACAACAAGGCGGAGTGGAGGTG
 CGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGATCTCAGCTTTAAGGA
 GCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAAAAGCTGACAGAGCA
 GTCCAACACCCCGCTTCTCTTGCTCTTGCTGCAAGAATGTCTGAGGAGTCTTACTTTGA
 ATCTAAAACAGAGGAGTCAAACAGTGCAGAGATGTATGTGATCAGATCACAGCAACAAGTAA
 CCGGGAGGGCCATGGCATGAACCCAAGTCTGCAGGCCATGATGCTGATGGGCTTTGGGGA
 TATCTTCTCAATGAACAAAGCAGGAGCTGTGATGCATTCTGGGATGCAGATAAACATGCA
 AGCCAAGCAGAATTCTTCCAAAACCACATCTAAGAGAAGGGGGAAGAAAGTCAACATGGC
 TCTGGGGTTTCAAGTATTTTGAAGTGTGACGATGATGATGATGATGACGGTGA
 GGAGGAGGATAATGACATGGATAATAGTGAATGAAAGCAGAAAGCAAAGTAATAAAATCA
 CAAATGTTTGGAAAACACAAAAGTAACCTGTTTATCTCAGTCTGTACAAAAACAGTAAGG
 AGGCAGAAAGCCAAGCACTGCATTTTTTAGGCCAATCACATTTACATGACCGTAATTTCTT
 ATCAATTCTACTTTTATTTTTGCTTACAGAAAAACGGGGGGAAGTAAGCCAAAGAAGT
 ATATTTATGAATCAGCAAATGTGGTGCCTGATTATAGAAATTTGTGATCCTATATACAAT
 ATAGGACTTTTTAAAGTTGTGACATTCTGGCTTTTTCTTTTAATGAATACTTTTTAGTTTG
 TATTTGACTTTATTTCTTTTATTCAAATCATTTTTAAAACTTACATTTTGAACAAACAC
 TCTTAACCTCTAATTGTTCTTTGACACGTAGTAATTCTGTGACATACTTTTTTTTTCTTA
 TAGCAATACACTGTAATATCAGAAATGGTTGGCCTGAGCAACCTAGTAAGACCTCGTCTC
 TACTAATAATTAAAAAACTAGCTGGCATGGTAGCACACCTGTAGTCCCAGATACTTGG
 GAGGCCAAGGCAGGAGGATTGCTTGAGACCTAGCAATCAGTCAGGGCTGCAGTGAGCCAT
 GATGGCACCCTGCACTCTAGCCTGGGCAAGAGAACAAAGATCCTGTCTCAAAAAACAAA
 AAAAAAAAAAAGGGCGGCCG

MSSLGASFVQIKFDDLQFFENC GGSGFSGSVYRAKWISQDKEVAVK
 KLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDM
 HIMTWATDVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRPHNHTHMS
 LVGTFPMMAPEVIQSLPVSETCDTYSYGVVLWEMLTREVPFKGLEGLQVAWLVEKNERL
 TIPSSCPRSFAELLHQWEADAKRPSFKQIISILESMSNDTSLPDKCNSFLHNKAEWRC
 EIEATLERLKKLERDLSFKBQELKERERRLKMWEQKLTBQSNTPLLLPLAARMSEESYFE
 SKTEESNSAEMSCQITATSNEGHGMNPSLQAMMLMGFGDIFSMNKAGAVMHSGMQINMQ
 AKQNSSKTTSKRRGKKVNMLGFSDFDLSEGGDDDDDDGEEEDNDMDNSE

FIGURE 2

CGGTGGTGGCGGCAGCGGCGGCTGCGGGGGCACCGGGCCGCGGCGCCACCATGGCCGTGC
 GACAGGCGCTGGGCGCGGGCCTGCAGCTGGGTGAGCGCTGCTGCTGCGCTTCACGGGCA
 AGCCCCGGCGGGCCTACGGCTTGGGGCGGCCGGGCCCCGGCGGGCGGTGTGTCCGCGGGG
 AGCGTCCAGGCTGGGCGCGAGGACCGGGCGCGAGCCTCGCAGGGTCGGGCTCGGGCTTC
 CTAACCGTCTCCGCTTCTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTTCAGCGGC
 AGTTTCGTGGTGGCGGCTGGGGCTGCGCGGGCCCTTGGCGGCGGGCAGTCTTCTGGCCT
 TCGGGCTAGGGCTGGGCCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGG
 CCTGTGAGGAGATCCAGGCAATTTTACCAGAAAAGCAAGCCGGGGCTGACCCGTTGG
 ACACGAGACGCTTGCAGGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTA
 AGGGCTGCAGTGCTGCTGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGG
 TGACAAAGAGCACCGGGTTGCTTCCAGGGAGAGGCCAGGTACCAGTGCACCAGGAGAAG
 GGCAGGAGCGAGTCCCGGGGCCCCCTGCCTTCCCTTGGCCATCAAGATGATGTGGAACA
 TCTCGGCAGGTTCTCCAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAG
 CGAGCCGAGTGGCTTGGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCAAGAGAG
 GTCCCAAGCAACTAGCCCCCTCACCCCAACATCATCCGGGTCTCCGCGCCTTACCTCTT
 CCGTGCCGCTGCTGCCAGGGGCCCTGGTCGACTACCTGATGTGCTGCCCTCACGCCTCC
 ACCCTGAAGGCTGGGCCATGGCCGGACGCTGTTCTCTGTTATGAAGAACTATCCCTGTA
 CCCTGCGCCAGTACCTTGTGTGAACACACCCAGCCCCCGCTCGCCGCCATGATGCTGC
 TGCAGCTGCTGGAAGGCGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGA
 AATCCGACAACATCCTTGTGGAGCTGGACCCAGACGGCTGCCCCCTGGCTGGTGTATCGCAG
 ATTTTGGCTGCTGCCCTGGCTGATGAGAGCATCGGCCCTGCAGTTGCCCTTCAGCAGCTGGT
 ACGTGGATCGGGGCGGAAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCTCTG
 GCCCCAGGGCAGTGATTGACTACAGCAAGGCTGATGCTGGGCAGTGGGAGCCATCGCCT
 ATGAAATCTTCGGGCTTGTCAATCCCTTCTACGGCCAGGGCAAGGCCACCTTGAAAGCC
 GCAGCTACCAAGAGGCTCAGCTACCTGCACTGCCCGAGTCAGTGCCTCCAGACGTGAGAC
 AGTTGGTGAGGGCACTGCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCCAGTAGCCG
 CAAATGTGCTTCATCTAAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGT
 TAGACAAGATGGTTGGCTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGC
 TCACAGAGAAGTGTGTGTGGAAACAAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGT
 GTGAAACGCTCTGCCAGGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTC
 CCTGCATGGAGCTGGTGAATTACTAAAAGAACTTGGCATCCTCTGTGTGCTGATGGTCTG
 TGAATGGTGAGGGTGGGAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAA
 AAGGCCTCGGGCTTGGCAAATGGAAGAACTTGAGTGAGAGTTCAGTCTGCAGTCTCTGTC
 TCACAGACATCTGAAAAGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGA
 GGGGTAGGCCTGCATCCACAGAGAGGATCCAGGCCAAGGCACTGGCTGTGAGTGGCAGAG
 TTTGGCTGTGACCTTTGCCCTTAACACGAGGAACCTCGTTTGAAGGGGGCAGCGTAGCATG
 TCTGATTTGCCACCTGGATGAAGGCAGACATCAACATGGGTGAGCACGTTTCAATTACGGG
 AGTGGGAAATTACATGAGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGC
 TACTGAATTATTAATCTCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTG
 GGGATTTAAACTTGAGGGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATAT
 TAAATGCAATTTACAACCTGCAAAAAAAGGGCGGCCCC

FIGURE 3

Met Ala

Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala Leu Leu
5 10 15

Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly Arg Pro
20 25 30

Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp Ala Ala
35 40 45 50

Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro Asn Arg
55 60 65

Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg Leu Gln
70 75 80

Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys Gly Arg
85 90 95

Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu Glu Lys
100 105 110

Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile Gln Ala
115 120 125 130

Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp Thr Arg
135 140 145

Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile
150 155 160

Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro Thr Leu
165 170 175

Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro Gly Arg
180 185 190

Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala Pro Gly
195 200 205 210

Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile Ser Ala
215 220 225

FIGURE 3 (cont'd)

Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu Leu Val
 230 235 240

Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val Thr Tyr
 245 250 255

Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro Asn Ile
 260 265 270

Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu Pro Gly
 275 280 285 290

Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His Pro Glu
 295 300 305

Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn Tyr Pro
 310 315 320

Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro Arg Leu
 325 330 335

Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His Leu Val
 340 345 350

Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile Leu Val
 355 360 365 370

Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp Phe Gly
 375 380 385

Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe Ser Ser
 390 395 400

Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro Glu Val
 405 410 415

Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser Lys Ala
 420 425 430

FIGURE 3 (cont'd)

Asp	Ala	Trp	Ala	Val	Gly	Ala	Ile	Ala	Tyr	Glu	Ile	Phe	Gly	Leu	Val
435					440				445					450	
Asn	Pro	Phe	Tyr	Gly	Gln	Gly	Lys	Ala	His	Leu	Glu	Ser	Arg	Ser	Tyr
			455					460						465	
Gln	Glu	Ala	Gln	Leu	Pro	Ala	Leu	Pro	Glu	Ser	Val	Pro	Pro	Asp	Val
			470				475						480		
Arg	Gln	Leu	Val	Arg	Ala	Leu	Leu	Gln	Arg	Glu	Ala	Ser	Lys	Arg	Pro
		485					490					495			
Ser	Ala	Arg	Val	Ala	Ala	Asn	Val	Leu	His	Leu	Ser	Leu	Trp	Gly	Glu
	500					505					510				
His	Ile	Leu	Ala	Leu	Lys	Asn	Leu	Lys	Leu	Asp	Lys	Met	Val	Gly	Trp
515					520					525					530
Leu	Leu	Gln	Gln	Ser	Ala	Ala	Thr	Leu	Leu	Ala	Asn	Arg	Leu	Thr	Glu
				535					540					545	
Lys	Cys	Cys	Val	Glu	Thr	Lys	Met	Lys	Met	Leu	Phe	Leu	Ala	Asn	Leu
			550					555					560		
Glu	Cys	Glu	Thr	Leu	Cys	Gln	Ala	Ala	Leu	Leu	Leu	Cys	Ser	Trp	Arg
		565					570					575			
Ala	Ala	Leu													

FIGURE 3 (cont'd)

GTCGACCCACGCGGTCCGCCCACGCGTTCCGGAGACATGTCTCTGTGTTTC
 TCTCCCCCTCCGCTTTTGAAGTCCGTTGAAGACACAATTTCTCTCTGTGCGGT
 GCTTAGGAGGAGCTCCATGAACATGTATTGAATTGGACTTAGCTGAACAG
 GCTGCTGGTTGGCTGCCAGAGGGGGCAGGCTGTGTTGCTGGGAGCCTTC
 CAGCTCCCTGCAGCAGTCATGGGGCAGGGTTCCCCGAGTCCGTAATCCCC
 ATTTCCACCTACTTTCCCTTAGTTATTTGATTCCCTGTCTGTCGTAATCAGC
 TTAAGTGGAGCATCCCCTTTCCTGGGAGACACGAAGCAGGAAACACTGGC
 AAATATCACAGCAGTGAGTTACGACTTTGATGAGGAATTCTTCAGCCAGA
 CGAGCGAGCTGGCCAAGGACTTTATTCGGAAGCTTCTGGTTAAAGAGACC
 CGGAAACGGCTCACAATCCAAGAGGCTCTCAGACACCCCTGGATCACGCC
 GGTGGACAACCAGCAAGCCATGGTGGCAGGGAGTCTGTGGTCAATCTGG
 AGAAGTTTCAGGAAGCAGTATGTCCGCAGGCGGTGGAAGCTTTCTTCAGC
 ATCGTGTCCCTGTGCAACCACCTACCCGCTCGCTGATGAAGAAGGTGCA
 CCTGAGGCCGGATGAGGACCTGAGGAACTGTGAGAGTGACACTGAGGAG
 GACATCGCCAGGAGGAAAGCCCTCCACCCACGGAGGAGGAGCAGCACCT
 CCTAACTGGCCTGACCTGCAGTGGCCGCCAGGGAGGTCTGGGCCCAGCGG
 GGCTCCCTTCTGTGCAGACTTTTGGACCCAGCTCAGCACCAGCACCCGGGC
 GTCCTGAGCACTTTGCAAGAGAGATGGGCCCAAGGAATTCAGAAGAGCTT
 GCAGGCAAGCCAGGAGACCCTGGGAGCTGTGGCTGTCTTCTGTGGAGGAG
 GCTCCAGCATTCCCAAAGCTCTTAATTCTCCATAAAATGGGCTTTCTCTGT
 TCTGCCATCCTCAGAGTCTGGGGTGGGAGTGTGGACTTAGGAAAACAATA
 TAAAGGACATCCTCATCATCACGGGGTGAAGGTGAGACTAAGGCAGCCTT
 CTTACAGGCTGAGGGGGTTTCAAGAACAGCCTGGCCAAAAATTACACCAG
 AGAGACAGAGTCCTCCCCATTGGGAACAGGGTGATTGAGGAAAGTGAACC
 TTGGGTGTGAGGGACCAATCCTGTGACCTCCCAGAACCATGGAAGCCAGG
 ACGTCAGGCTGACCAACACCTCAGACCTTCTGAAGCAGCCCATTGCTGGC
 CCGCCATGTTGTAATTTTGTCTATTTTATTAACTTCTGGTTTACCTGATG
 CTTGGCTTCTTTTAGGGCTACCCCCATCTCATTTCCTTTAGCCCGTGTGCCT
 GTAACCTGTGAGGGGGGGCACCCAGTGGGGTGCTGAGTGGGCAGAATCTCA
 GAAGGTCTCTGAACCGTCCGCGCAGGCCTGCAGTGGGCCTGCCTCCTC
 CTTGCTTCCCTAACAGGAAGGTGTCCAGTTCAAGAGAACCCACCCAGAGA
 CTGGGAGTGGTGGCTCACGCCTATAATCCCTGCGCTTTGGCAGTCCGAGG
 CAGGGGAATTGCTTGAAGTCAAGAGTGGAGACCAGCCTGGGCAACATGG
 CAAAACGCAGTCTGTACAAAAAATACAAAAAATTAGCCAGGTGTAGGGGT
 AGGCACCTGGCATCCAGCTACTCCAGGGGCTGAGGTGACAGCATTGCTT
 AAGCCCAGAAGGTGAGGCTGCAGTGAGCTGAGATCACGCCACTGCACTC
 CAGTCTGGGTGACAGAGAGAGACCATATCCAAAAAAGGG
 CCGCCGC

LFDLSVVLSSGASPLGDTKQETLANITAVSYDFDEEFFSQTSELAKDFIRKL
 LVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQYVRRRWK
 LSFSIVSLCNHLTRSLMKKVHLRPDEDLRNCESDTEEDIARRKALHPRRSSTS

FIGURE 4

T A L A K E L R E L R I E E T N R P M 19
 G ACG GCA TTA GCC AAA GAA CTA AGA GAA CTC CGG ATT GAA GAA ACA AAC CGC CCA ATG 57
 K K V T D Y S S S S B E S E S S E E E E 39
 AAG AAG GTG ACT GAT TAC TCC TCC TCC AGT GAG GAG TCA GAA AGT AGC GAG GAA GAG GAG 117
 E D G E S E T H D G T V A V S D I P R L 59
 GAA GAT GGA GAG AGC GAG ACC CAT GAT GGG ACA GTG GCT GTC AGC GAC ATA CCC AGA CTG 177
 I P T G A P G S N E Q Y N V G M V G T H 79
 ATA CCA ACA GGA GCT CCA GGC AGC AAC GAG CAG TAC AAT GTG GGA ATG GTG GGG AGC CAT 237
 G L E T S H A D S F S G S I S R E G T L 99
 GGG CTG GAG ACC TCT CAT GCG GAC AGT TTC AGC GGC AGT ATT TCA AGA GAA GGA ACC TTG 297
 M I R E T S G E K K R S G H S D S N G F 119
 ATG ATT AGA GAG ACG TCT GGA GAG AAG AAG CGA TCT GGC CAC AGT GAC AGC AAT GGC TTT 357
 A G H I N L P D L V Q Q S H S P A G T P 139
 GCT GGC CAC ATC AAC CTC OCT GAC CTG GTG CAG CAG AGC CAT TCT CCA GCT GGA ACC CCG 417
 T E G L G R V S T H S Q E M D S G T E Y 159
 ACT GAG GGA CTG GGG GGC GTC TCA ACC CAT TCC CAG GAG ATG GAC TCT GGG ACT GAA TAT 477
 G A G S S T R A S F T P F V D P R V Y Q 179
 GGC ATG GGG AGC AGC ACC AAA GGC TCC TTC ACC CCC TTT GTG GAC CCC AGA GTA TAC CAG 537
 T S P T D E D E D E E S S A A A L F T 199
 ACG TCT CCC ACT GAT GAA GAT GAA GAG GAT GAG GAA TCA TCA GGC GCA GCT CTG TTT ACT 597
 S E L L R Q E Q A K L N E A R K I S V V 219
 AGC GAA CTT CTT AGG CAA GAA CAG GGC AAA CTC AAT GAA GCA AGA AAG ATT TCG GTG GTA 657
 N V N P T N I R P H S D T P E I R K Y K 239
 AAT GTA AAC CCA ACC AAC ATT CCG OCT CAT AGC GAC ACA CCA GAA ATC AGA AAA TAC AAG 717
 K R F N S E I L C A A L W G V N L L V G 259
 AAA CGA TTC AAC TCA GAA ATA CTT TGT GCA GCT CTG TGG GGT GTA AAC CTT CTG GTG GGG 777
 T E N G L M L L D R S G Q G K V Y N L I 279
 ACT GAA AAT GGC CTG ATG CTT TTG GAC CGA AGT GGG CAA GGC AAA GTC TAT AAT CTG ATC 837
 N R R R F Q Q M D V L E G L N V L V T I 299
 AAC CCG AGG CGA TTT CAG CAG ATG GAT GTG CTA GAG GGA CTG AAT GTC CTT GTG ACA ATT 897
 S G K K N K L R V Y Y L S W L R N R I L 319
 TCA GGA AAG AAG AAT AAG CTA CGA GTT TAC TAT CTT TCA TGG TTA AGA AAC AGA ATA CTA 957
 H N D P E V E K K Q G W I T V G D L E G 339
 CAT AAT GAC CCA GAA GTA GAA AAG AAA CAA GGC TGG ATC ACT GTT GGG GAC TTG GAA GGC 1017
 C I H Y K V V K Y E R I K F L V I A L K 359
 TGT ATA CAT TAT AAA GIT GTT AAA TAT GAA AGG ATC AAA TTT TTG GTG ATT GCC TTA AAG 1077
 N A V E I Y A W A P K P Y H K F M A F K 379
 AAT GCT GTG GAA ATA TAT GCT TGG GCT OCT AAA CCG TAT CAT AAA TTC ATG GCA TTT AAG 1137
 S F A D L Q H K P L L V D L T V E E G Q 399
 TCT TTT GCA GAT CTC CAG CAC AAG OCT CTG CTA GTT GAT CTC ACG GTA GAA GAA GGT CAA 1197
 R L K V I F G S H T G F H V I D V D S G 419

FIGURE 5

AGA	TTA	AAG	GTT	ATT	TTT	GGT	TCA	CAC	ACT	GGT	TTC	CAT	GTA	ATT	GAT	GTT	GAT	TCA	GGA	1257
N	S	Y	D	I	Y	I	P	S	H	I	Q	G	N	I	T	P	H	A	I	439
AAC	TCT	TAT	GAT	ATC	TAC	ATA	CCA	TCT	CAT	ATT	CAG	GGC	AAT	ATC	ACT	CCT	CAT	GCT	ATT	1317
V	I	L	P	K																444
GTC	ATC	TIG	CCT	AAA																1332

FIGURE 5 (cont'd)